

1/13

SEQUENCE LISTING

<110> THE SIR MORTIMER B. DAVIS-JEWISH GENERAL HOSPITAL

<120> HIGHLY ACTIVE FORMS OF INTERFERON REGULATORY FACTOR

PROTEINS

<130> IRF-3

<140>

<141>

<150> CA 2,234,588

<151> 1998-04-07

<160> 11

<170> PatentIn Ver. 2.0

<210> 1

<211> 1284

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (1281)

<400> 1

atg	gga	acc	cca	aag	cca	cgg	atc	ctg	ccc	tgg	ctg	gtg	tcg	cag	ctg	48
Met	Gly	Thr	Pro	Lys	Pro	Arg	Ile	Leu	Pro	Trp	Leu	Val	Ser	Gln	Leu	
1				5				10						15		

gac	ctg	ggg	caa	ctg	gag	ggc	gtg	gcc	tgg	gtg	aac	aag	agc	cgc	acg	96
Asp	Leu	Gly	Gln	Leu	Glu	Gly	Val	Ala	Trp	Val	Asn	Lys	Ser	Arg	Thr	
		20						25					30			

cgc	ttc	cgc	atc	cct	tgg	aag	cac	ggc	cta	cgg	cag	gat	gca	cag	cag	144
Arg	Phe	Arg	Ile	Pro	Trp	Lys	His	Gly	Leu	Arg	Gln	Asp	Ala	Gln	Gln	
		35					40					45				

gag	gat	ttc	gga	atc	ttc	cag	gcc	tgg	gcc	gag	gcc	act	ggt	gca	tat	192
Glu	Asp	Phe	Gly	Ile	Phe	Gln	Ala	Trp	Ala	Glu	Ala	Thr	Gly	Ala	Tyr	
	50					55				60						

gtt	ccc	ggg	agg	gat	aag	cca	gac	ctg	cca	acc	tgg	aag	agg	aat	ttc	240
Val	Pro	Gly	Arg	Asp	Lys	Pro	Asp	Leu	Pro	Thr	Trp	Lys	Arg	Asn	Phe	
	65				70					75					80	

T014250" 55624960

2/13

cgc tct gcc ctc aac cgc aaa gaa ggg ttg cgt tta gca gag gac cgg 288
 Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
 85 90 95

agc aag gac cct cac gac cca cat aaa atc tac gag ttt gtg aac tca 336
 Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
 100 105 110

gga gtt ggg gac ttt tcc cag cca gac acc tct ccg gac acc aat ggt 384
 Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
 115 120 125

gga ggc agt act tct gat acc cag gaa gac att ctg gat gag tta ctg 432
 Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
 130 135 140

ggt aac atg gtg ttg gcc cca ctc cca gat ccg gga ccc cca agc ctg 480
 Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
 145 150 155 160

gct gta gcc cct gag ccc tgc cct cag ccc ctg cgg agc ccc agc ttg 528
 Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
 165 170 175

gac aat ccc act ccc ttc cca aac ctg ggg ccc tct gag aac cca ctg 576
 Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
 180 185 190

aag cgg ctg ttg gtg ccg ggg gaa gag tgg gag ttc gag gtg aca gcc 624
 Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala
 195 200 205

ttc tac cgg ggc cgc caa gtc ttc cag cag acc atc tcc tgc ccg gag 672
 Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
 210 215 220

ggc ctg cgg ctg gtg ggg tcc gaa gtg gga gac agg acg ctg cct gga 720
 Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
 225 230 235

tgg cca gtc aca ctg cca gac cct ggc atg tcc ctg aca gac agg gga 768
 Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
 240 245 250 255

gtg atg agc tac gtg agg cat gtg ctg agc tgc ctg ggt ggg gga ctg 816
 Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
 260 265 270

gct ctc tgg cgg gcc ggg cag tgg ctc tgg gcc cag cgg ctg ggg cac 864
 Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
 275 280 285

tgc cac aca tac tgg gca gtg agc gag gag ctg ctc ccc aac agc ggg 912
 Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
 290 295 300

cat ggg cct gat ggc gag gtc ccc aag gac aag gaa gga ggc gtg ttt 960
 His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
 305 310 315

gac ctg ggg ccc ttc att gta gat ctg att acc ttc acg gaa gga agc 1008
 Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
 320 325 330 335

gga cgc tca cca cgc tat gcc ctc tgg ttc tgt gtg ggg gag tca tgg 1056
 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
 340 345 350

F04250-59624960

3/13

ccc cag gac cag ccg tgg acc aag agg ctc gtg atg gtc aag gtt gtg 1104
 Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
 355 360 365

ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta ggg ggt gcc 1152
 Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
 370 375 380

tcc tcc ctg gag aat act gtg gac ctg cac att gac aac gac cac cca 1200
 Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
 385 390 395

ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag gac ttg gtg 1248
 Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
 400 405 410 415

gag ggc atg gat ttc cag ggc cct ggg gag agc tga 1284
 Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
 420 425

<210> 2

<211> 427

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu
 1 5 10 15

Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr
 20 25 30

Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln
 35 40 45

Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
 50 55 60

Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
 65 70 75

Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
 80 85 90 95

Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
 100 105 110

Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
 115 120 125

Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
 130 135 140

Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
 145 150 155

Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
 160 165 170 175

Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
 180 185 190

T04250:59624960

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

[illegible][illegible]

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

[illegible]

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

[illegible]

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

D **E** **F** **G** **H** **I** **J** **K** **L** **M** **N** **O** **P** **Q** **R** **S** **T** **U** **V** **W** **X** **Y** **Z**

5/13

Gly Ala Ala Ala
1

<210> 5

<211> 6

<212> PRT

<213> Homo sapiens

<400> 5

Gly Ala Ala Ala Asn Asn
1 5

<210> 6

<211> 15

<212> DNA

<213> Homo sapiens

<400> 6

ggaaaactga aaggg

15

<210> 7

<211> 30

<212> DNA

<213> Homo sapiens

<400> 7

gatcgggaaa gggaaaccga aactgaagcc

30

<210> 8

<211> 1512

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1509)

<400> 8

atg gcc ttg gct cct gag agg gca gcc cca cgc gtg ctg ttc gga gag	48
Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu	
1 5 10 15	

tgg ctc ctt gga gag atc agc agc ggc tgc tat gag ggg ctg cag tgg	96
Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp	
20 25 30	

Publ. No. 99/00314

6/13

ctg gac gag gcc cgc acc tgt ttc cgc gtg ccc tgg aag cac ttc gcg 144
 Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45

cgc aag gac ctg agc gag gcc gac gcg cgc atc ttc aag gcc tgg gct 192
 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60

gtg gcc cgc ggc agg tgg ccg cct agc agc agg gga ggt ggc ccg ccc 240
 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80

ccc gag gct gag act gcg gag cgc gcc ggc tgg aaa acc aac ttc cgc 288
 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95

tgc gca ctg cgc agc acg cgt cgc ttc gtg atg ctg cgg gat aac tcg 336
 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
 100 105 110

ggg gac ccg gcc gac ccg cac aag gtg tac gcg ctc agc cgg gag ctg 384
 Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
 115 120 125

tgc tgg cga gaa ggc cca ggc acg gac cag act gag gca gag gcc ccc 432
 Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
 130 135 140

gca gct gtc cca cca cca cag ggt ggg ccc cca ggg cca ttc ttg gca 480
 Ala Ala Val Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
 145 150 155 160

cac aca cat gct gga ctc caa gcc cca ggc ccc ctc cct gcc cca gct 528
 His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
 165 170 175

ggt gac aag ggg gac ctc ctg ctc cag gca gtg caa cag agc tgc ctg 576
 Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
 180 185 190

gca gac cat ctg ctg aca gcg tca tgg ggg gca gat cca gtc cca acc 624
 Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
 195 200 205

aag gct cct gga gag gga caa gaa ggg ctt ccc ctg act ggg gcc tgt 672
 Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
 210 215 220

gct gga ggc cca ggg ctc cct gct ggg gag ctg tac ggg tgg gca gta 720
 Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
 225 230 235 240

gag acg acc ccc agc ccc ggg ccc cag ccc gcg gca cta acg aca ggc 768
 Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
 245 250 255

gag gcc gcg gcc cca gag tcc ccg cac cag gca gag ccg tac ctg tca 816
 Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
 260 265 270

ccc tcc cca agc gcc tgc acc gcg gtg caa gag ccc agc cca ggg gcg 864
 Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
 275 280 285

ctg gac gtg acc atc atg tac aag ggc cgc acg gtg ctg cag aag gtg 912
 Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
 290 295 300

T 0 4 2 5 0 : 5 9 6 2 4 9 6 0

7/13

gtg gga cac ccg agc tgc acg ttc cta tac ggc ccc cca gac cca gct 960
 Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
 305 310 315 320

gtc cgg gcc aca gac ccc cag cag gta gca ttc ccc agc cct gcc gag 1008
 Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
 325 330 335

ctc ccg gac cag aag cag ctg cgc tac acg gag gaa ctg ctg cgg cac 1056
 Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
 340 345 350

gtg gcc cct ggg ttg cac ctg gag ctt cgg ggg cca cag ctg tgg gcc 1104
 Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
 355 360 365

cgg cgc atg ggc aag tgc aag gtg tac tgg gag gtg ggc gga ccc cca 1152
 Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
 370 375 380

ggc tcc gcc agc ccc tcc acc cca gcc tgc ctg ctg cct cgg aac tgt 1200
 Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
 385 390 395 400

gac acc ccc atc ttc gac ttc aga gtc ttc ttc caa gag ctg gtg gaa 1248
 Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
 405 410 415

ttc cgg gca cgg cag cgc cgt ggc tcc cca cgc tat acc atc tac ctg 1296
 Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
 420 425 430

ggc ttc ggg cag gac ctg tca gct ggg agg ccc aag gag aag agc ctg 1344
 Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
 435 440 445

gtc ctg gtg aag ctg gaa ccc tgg ctg tgc cga gtg cac cta gag ggc 1392
 Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
 450 455 460

acg cag cgt gag ggt gtg tct tcc ctg gat agc agc gac ctc gac ctc 1440
 Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Asp Leu Asp Leu
 465 470 475 480

tgc ctg tcc agc gcc aac agc ctc tat gac gac atc gag tgc ttc ctt 1488
 Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu
 485 490 495

atg gag ctg gag cag ccc gcc tag 1512
 Met Glu Leu Glu Gln Pro Ala
 500

<210> 9

<211> 503

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
 1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
 20 25 30

T04250-59641960

8/13

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45
 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60
 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80
 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95
 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
 100 105 110
 Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu
 115 120 125
 Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro
 130 135 140
 Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala
 145 150 155 160
 His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala
 165 170 175
 Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu
 180 185 190
 Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr
 195 200 205
 Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys
 210 215 220
 Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Leu Tyr Gly Trp Ala Val
 225 230 235 240
 Glu Thr Thr Pro Ser Pro Gly Pro Gln Pro Ala Ala Leu Thr Thr Gly
 245 250 255
 Glu Ala Ala Ala Pro Glu Ser Pro His Gln Ala Glu Pro Tyr Leu Ser
 260 265 270
 Pro Ser Pro Ser Ala Cys Thr Ala Val Gln Glu Pro Ser Pro Gly Ala
 275 280 285
 Leu Asp Val Thr Ile Met Tyr Lys Gly Arg Thr Val Leu Gln Lys Val
 290 295 300
 Val Gly His Pro Ser Cys Thr Phe Leu Tyr Gly Pro Pro Asp Pro Ala
 305 310 315 320
 Val Arg Ala Thr Asp Pro Gln Gln Val Ala Phe Pro Ser Pro Ala Glu
 325 330 335
 Leu Pro Asp Gln Lys Gln Leu Arg Tyr Thr Glu Glu Leu Leu Arg His
 340 345 350
 Val Ala Pro Gly Leu His Leu Glu Leu Arg Gly Pro Gln Leu Trp Ala
 355 360 365
 Arg Arg Met Gly Lys Cys Lys Val Tyr Trp Glu Val Gly Gly Pro Pro
 370 375 380
 Gly Ser Ala Ser Pro Ser Thr Pro Ala Cys Leu Leu Pro Arg Asn Cys
 385 390 395 400

F01250" 5364960

9/13

Asp Thr Pro Ile Phe Asp Phe Arg Val Phe Phe Gln Glu Leu Val Glu
 405 410 415
 Phe Arg Ala Arg Gln Arg Arg Gly Ser Pro Arg Tyr Thr Ile Tyr Leu
 420 425 430
 Gly Phe Gly Gln Asp Leu Ser Ala Gly Arg Pro Lys Glu Lys Ser Leu
 435 440 445
 Val Leu Val Lys Leu Glu Pro Trp Leu Cys Arg Val His Leu Glu Gly
 450 455 460
 Thr Gln Arg Glu Gly Val Ser Ser Leu Asp Ser Ser Asp Leu Asp Leu
 465 470 475 480
 Cys Leu Ser Ser Ala Asn Ser Leu Tyr Asp Asp Ile Glu Cys Phe Leu
 485 490 495
 Met Glu Leu Glu Gln Pro Ala
 500

<210> 10

<211> 1629

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1626)

<400> 10

atg gcc ttg gct cct gag agg gca gcc cca cgc gtg ctg ttc gga gag 48
 Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
 1 5 10 15
 tgg ctc ctt gga gag atc agc agc ggc tgc tat gag ggg ctg cag tgg 96
 Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
 20 25 30
 ctg gac gag gcc cgc acc tgt ttc cgc gtg ccc tgg aag cac ttc gcg 144
 Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45
 cgc aag gac ctg agc gag gcc gac gcg cgc atc ttc aag gcc tgg gct 192
 Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60
 gtg gcc cgc ggc agg tgg ccg cct agc agc agg gga ggt ggc ccg ccc 240
 Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80
 ccc gag gct gag act gcg gag cgc gcc ggc tgg aaa acc aac ttc cgc 288
 Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95
 tgc gca ctg cgc agc acg cgt cgc ttc gtg atg ctg cgg gat aac tcg 336
 Cys Ala Leu Arg Ser Thr Arg Arg Phe Val Met Leu Arg Asp Asn Ser
 100 105 110

T 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0

10/13

ggg gac ccg gcc gac ccg cac aag gtg tac gcg ctc agc cgg gag ctg	384
Gly Asp Pro Ala Asp Pro His Lys Val Tyr Ala Leu Ser Arg Glu Leu	
115 120 125	
tgc tgg cga gaa ggc cca ggc acg gac cag act gag gca gag gcc ccc	432
Cys Trp Arg Glu Gly Pro Gly Thr Asp Gln Thr Glu Ala Glu Ala Pro	
130 135 140	
gca gct gtc cca cca cca cag ggt ggg ccc cca ggg cca ttc ttg gca	480
Ala Ala Val Pro Pro Pro Gln Gly Gly Pro Pro Gly Pro Phe Leu Ala	
145 150 155 160	
cac aca cat gct gga ctc caa gcc cca ggc ccc ctc cct gcc cca gct	528
His Thr His Ala Gly Leu Gln Ala Pro Gly Pro Leu Pro Ala Pro Ala	
165 170 175	
ggt gac aag ggg gac ctc ctg ctc cag gca gtg caa cag agc tgc ctg	576
Gly Asp Lys Gly Asp Leu Leu Leu Gln Ala Val Gln Gln Ser Cys Leu	
180 185 190	
gca gac cat ctg ctg aca gcg tca tgg ggg gca gat cca gtc cca acc	624
Ala Asp His Leu Leu Thr Ala Ser Trp Gly Ala Asp Pro Val Pro Thr	
195 200 205	
aag gct cct gga gag gga caa gaa ggg ctt ccc ctg act ggg gcc tgt	672
Lys Ala Pro Gly Glu Gly Gln Glu Gly Leu Pro Leu Thr Gly Ala Cys	
210 215 220	
gct gga ggc cca ggg ctc cct gct ggg gag ctg tac ggg tgg gca gta	720
Ala Gly Gly Pro Gly Leu Pro Ala Gly Glu Tyr Gly Trp Ala Val	
225 230 235 240	
gag acg acc ccc agc ccc act tct gat acc cag gaa gac att ctg gat	768
Glu Thr Thr Pro Ser Pro Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp	
245 250 255	
gag tta ctg ggt aac atg gtg ttg gcc cca ctc cca gat ccg gga ccc	816
Glu Leu Leu Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro	
260 265 270	
cca agc ctg gct gta gcc cct gag ccc tgc cct cag ccc ctg cgg agc	864
Pro Ser Leu Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser	
275 280 285	
ccc agc ttg gac aat ccc act ccc ttc cca aac ctg ggg ccc tct gag	912
Pro Ser Leu Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu	
290 295 300	
aac cca ctg aag cgg ctg ttg gtg ccg ggg gaa gag tgg gag ttc gag	960
Asn Pro Leu Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu	
305 310 315 320	
gtg aca gcc ttc tac ccg ggc cgc caa gtc ttc cag cag acc atc tcc	1008
Val Thr Ala Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser	
325 330 335	
tgc ccg gag ggc ctg ccg ctg gtg ggg tcc gaa gtg gga gac agg acg	1056
Cys Pro Glu Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr	
340 345 350	
ctg cct gga tgg cca gtc aca ctg cca gac cct ggc atg tcc ctg aca	1104
Leu Pro Gly Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr	
355 360 365	
gac agg gga gtg atg agc tac gtg agg cat gtg ctg agc tgc ctg ggt	1152
Asp Arg Gly Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly	
370 375 380	

T01050-33624950

11/13

ggg gga ctg gct ctc tgg cgg gcc ggg cag tgg ctc tgg gcc cag cgg 1200
 Gly Gly Leu Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg
 385 390 395 400

ctg ggg cac tgc cac aca tac tgg gca gtg agc gag gag ctg ctc ccc 1248
 Leu Gly His Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro
 405 410 415

aac agc ggg cat ggg cct gat ggc gag gtc ccc aag gac aag gaa gga 1296
 Asn Ser Gly His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly
 420 425 430

ggc gtg ttt gac ctg ggg ccc ttc att gta gat ctg att acc ttc acg 1344
 Gly Val Phe Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr
 435 440 445

gaa gga agc gga cgc tca cca cgc tat gcc ctc tgg ttc tgt gtg ggg 1392
 Glu Gly Ser Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly
 450 455 460

gag tca tgg ccc cag gac cag ccg tgg acc aag agg ctc gtg atg gtc 1440
 Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val
 465 470 475 480

aag gtt gtg ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta 1488
 Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val
 485 490 495

ggg ggt gcc tcc tcc ctg gag aat act gtg gac ctg cac att gac aac 1536
 Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn
 500 505 510

gac cac cca ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag 1584
 Asp His Pro Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln
 515 520 525

gac ttg gtg gag ggc atg gat ttc cag ggc cct ggg gag agc tga 1629
 Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
 530 535 540

<210> 11

<211> 542

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Ala Pro Glu Arg Ala Ala Pro Arg Val Leu Phe Gly Glu
 1 5 10 15

Trp Leu Leu Gly Glu Ile Ser Ser Gly Cys Tyr Glu Gly Leu Gln Trp
 20 25 30

Leu Asp Glu Ala Arg Thr Cys Phe Arg Val Pro Trp Lys His Phe Ala
 35 40 45

Arg Lys Asp Leu Ser Glu Ala Asp Ala Arg Ile Phe Lys Ala Trp Ala
 50 55 60

Val Ala Arg Gly Arg Trp Pro Pro Ser Ser Arg Gly Gly Gly Pro Pro
 65 70 75 80

Pro Glu Ala Glu Thr Ala Glu Arg Ala Gly Trp Lys Thr Asn Phe Arg
 85 90 95

T01250" 59644960

THE **WORLD'S** **LARGEST** **BOOK** **STORE**

[illegible]

13/13

Glu Ser Trp Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val
465 470 475 480

Lys Val Val Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val
485 490 495

Gly Gly Ala Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn
500 505 510

Asp His Pro Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln
515 520 525

Asp Leu Val Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
530 535 540

T01230" 59624960

2/13

10

20

40 30 20 10 0

50

60

gga cgc tca cca cgc tat gcc ctc tgg ttc tgt gtg ggg gag tca tgg 1056
 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
 340 345 350

3/13

ccc cag gac cag ccg tgg acc aag agg ctc gtg atg gtc aag gtt gtg 1104
Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
355 360 365

ccc acg tgc ctc agg gcc ttg gta gaa atg gcc cgg gta ggg ggt gcc 1152
Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
370 375 380

10 tcc tcc ctg gag aat act gtg gac ctg cac att gac aac gac cac cca 1200
Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
385 390 395 400

ctc gac ctc gac gac gac cag tac aag gcc tac ctg cag gac ttg gtg 1248
Leu Asp Leu Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
405 410 415

gag ggc atg gat ttc cag ggc cct ggg gag agc tga 1284
Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
420 425

20

<210> 2

<211> 427

<212> PRT

<213> Homo sapiens

<400> 2

Met Gly Thr Pro Lys Pro Arg Ile Leu Pro Trp Leu Val Ser Gln Leu
1 5 10 15

Asp Leu Gly Gln Leu Glu Gly Val Ala Trp Val Asn Lys Ser Arg Thr
20 25 30

Arg Phe Arg Ile Pro Trp Lys His Gly Leu Arg Gln Asp Ala Gln Gln
35 40 45

Glu Asp Phe Gly Ile Phe Gln Ala Trp Ala Glu Ala Thr Gly Ala Tyr
50 55 60

Val Pro Gly Arg Asp Lys Pro Asp Leu Pro Thr Trp Lys Arg Asn Phe
65 70 75 80

40

Arg Ser Ala Leu Asn Arg Lys Glu Gly Leu Arg Leu Ala Glu Asp Arg
85 90 95

Ser Lys Asp Pro His Asp Pro His Lys Ile Tyr Glu Phe Val Asn Ser
100 105 110

Gly Val Gly Asp Phe Ser Gln Pro Asp Thr Ser Pro Asp Thr Asn Gly
115 120 125

50

Gly Gly Ser Thr Ser Asp Thr Gln Glu Asp Ile Leu Asp Glu Leu Leu
130 135 140

Gly Asn Met Val Leu Ala Pro Leu Pro Asp Pro Gly Pro Pro Ser Leu
145 150 155 160

Ala Val Ala Pro Glu Pro Cys Pro Gln Pro Leu Arg Ser Pro Ser Leu
165 170 175

60

Asp Asn Pro Thr Pro Phe Pro Asn Leu Gly Pro Ser Glu Asn Pro Leu
180 185 190

ART 34 AMDT

M105.00.00
4/13

Lys Arg Leu Leu Val Pro Gly Glu Glu Trp Glu Phe Glu Val Thr Ala
 195 200 205
 Phe Tyr Arg Gly Arg Gln Val Phe Gln Gln Thr Ile Ser Cys Pro Glu
 210 215 220
 Gly Leu Arg Leu Val Gly Ser Glu Val Gly Asp Arg Thr Leu Pro Gly
 225 230 235 240
 10 Trp Pro Val Thr Leu Pro Asp Pro Gly Met Ser Leu Thr Asp Arg Gly
 245 250 255
 Val Met Ser Tyr Val Arg His Val Leu Ser Cys Leu Gly Gly Gly Leu
 260 265 270
 Ala Leu Trp Arg Ala Gly Gln Trp Leu Trp Ala Gln Arg Leu Gly His
 275 280 285
 20 Cys His Thr Tyr Trp Ala Val Ser Glu Glu Leu Leu Pro Asn Ser Gly
 290 295 300
 His Gly Pro Asp Gly Glu Val Pro Lys Asp Lys Glu Gly Gly Val Phe
 305 310 315 320
 Asp Leu Gly Pro Phe Ile Val Asp Leu Ile Thr Phe Thr Glu Gly Ser
 325 330 335
 Gly Arg Ser Pro Arg Tyr Ala Leu Trp Phe Cys Val Gly Glu Ser Trp
 340 345 350
 Pro Gln Asp Gln Pro Trp Thr Lys Arg Leu Val Met Val Lys Val Val
 355 360 365
 Pro Thr Cys Leu Arg Ala Leu Val Glu Met Ala Arg Val Gly Gly Ala
 370 375 380
 Ser Ser Leu Glu Asn Thr Val Asp Leu His Ile Asp Asn Asp His Pro
 385 390 395 400
 40 Leu Asp Leu Asp Asp Asp Gln Tyr Lys Ala Tyr Leu Gln Asp Leu Val
 405 410 415
 Glu Gly Met Asp Phe Gln Gly Pro Gly Glu Ser
 420 425

<210> 3

<211> 13

<212> PRT

<213> Homo sapiens

50 <400> 3

Ile Ser Asn Ser His Pro Leu Ser Leu Thr Ser Asp Gln
 1 5 10

<210> 4

<211> 4

<212> PRT

<213> Homo sapiens

<400> 4

444

AMENDED SHEET